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DOCUMENT-IDENTIFIER: US 5372928 A

TITLE: Hepatitis C virus isolates

DATE-ISSUED: December 13, 1994

INVENTOR-INFORMATION:

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US-CL-CURRENT: 435/5,435/6 ,536/23.72 ,536/24.32

CLAIMS:

We claim:

1. A method of detecting an hepatitis C virus (HCV) polynucleotide in a test sample, if any, comprising:
  - (a) providing a probe comprising a polynucleotide containing a sequence of at least 15 bp from an HCV isolate selected from the group of J1 and J7, wherein said sequence is not homologous to the sequence of HCV isolate HCV1, wherein the sequence is complementary to a sequence in the HCV polynucleotide to be detected, and wherein the sequence is from a J1 or J7 sequence in FIG. 1, FIG. 3, FIG. 4, FIG. 5, FIG. 7, FIG. 8, FIG. 9, FIG. 10, FIG. 13, FIG. 14, FIG. 15, FIG. 16, FIG. 17, FIG. 18, FIG. 19 or FIG. 1;
  - (b) contacting the test sample and the probe under conditions that allow for the formation of a polynucleotide duplex between the probe and its complement, if any, in the absence of substantial polynucleotide duplex formation between the probe and non-HCV polynucleotide sequences present in the test sample, if any; and
  - (c) detecting any polynucleotide duplexes comprising the probe.
2. A method of detecting in a test sample a polynucleotide containing a sequence from an hepatitis C virus (HCV) polynucleotide, if any, the method comprising:
  - (a) providing a probe comprising a polynucleotide containing a sequence of at least 15 bp from an HCV isolate J1, wherein said sequence is not homologous to the nucleotide sequence of HCV isolate HCV1, wherein the J1 sequence is from a J1 polynucleotide sequence in FIG. 2, FIG. 3, FIG. 4, FIG. 5, FIG. 7, FIG. 8, FIG. 9, FIG. 10, FIG. 13, FIG. 14, FIG. 15, FIG. 16, FIG. 17, FIG. 18, or FIG. 19, and wherein the sequence is complementary to a sequence in the HCV polynucleotide to be detected;
  - (b) contacting the test sample and the probe under conditions that allow for the

formation of a polynucleotide duplex between the probe and its complement, if any, in the absence of substantial polynucleotide duplex formation between the probe and non-HCV polynucleotide sequences present in the test sample, if any; and  
(c) detecting any polynucleotide duplexes comprising the probe.

3. A method of detecting in a test sample a polynucleotide containing a sequence from an hepatitis C virus (HCV) polynucleotide, if any, the method comprising:

(a) providing a probe comprising a polynucleotide containing a sequence of at least 15 bp from an HCV isolate J7, wherein said sequence is not homologous to the nucleotide sequence of HCV isolate HCV1, wherein the J7 sequence is from a J7 polynucleotide sequence in FIG. 1 or FIG. 7, and wherein the sequence is complementary to a sequence in the HCV polynucleotide to be detected;  
(b) contacting the test sample and the probe under conditions that allow for the formation of a polynucleotide duplex between the probe and its complement, if any, in the absence of substantial polynucleotide duplex formation between the probe and non-HCV polynucleotide sequences present in the test sample, if any; and  
(c) detecting any polynucleotide duplexes comprising the probe.

4. The method of claim 1 wherein the J1 or J7 sequence is from HCV polynucleotides deposited under Accession Numbers BP-2593, BP-2594, BP-2595, BP-2637, BP-2638, BP-3081, ATCC No. 68392, ATCC No. 68393, ATCC No. 68394, ATCC No. 68395, and ATCC

No. 40884.

5. The method of claim 2 wherein the J1 or J7 sequence is from HCV polynucleotides deposited under Accession Numbers BP-2593, BP-2594, BP-2595, BP-b 2637, BP-2638, BP-3081, ATCC No. 68392, ATCC No. 68393, ATCC No. 68394, ATCC No. 68395, and ATCC

No. 40884.

6. The method of claim 3 wherein the J1 or J7 sequence is from HCV polynucleotides deposited under Accession Numbers BP-2593, BP-2594, BP-2595, BP-2637, BP-2638, BP-3081, ATCC No. 68392, ATCC No. 68393, ATCC No. 68394, ATCC No. 68395, and ATCC

No. 40884.

US-PAT-NO: 5350671

DOCUMENT-IDENTIFIER: US 5350671 A

TITLE: HCV immunoassays employing C domain antigens

DATE-ISSUED: September 27, 1994

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
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Choo; Qui-Lim	El Cerrito	CA	N/A	N/A
Kuo; George	San Francisco	CA	N/A	N/A

US-CL-CURRENT: 435/5,435/6 ,435/975 ,436/512 ,436/518 ,530/300 ,530/326 ,530/327  
,530/328 ,530/812 ,530/826 ,930/220 ,930/223

CLAIMS:

We claim:

1. An immunoassay for detecting antibodies that bind to a hepatitis C virus (HCV) polypeptide comprising:
  - (a) providing an antigen comprising the C domain polypeptide encoded by HCV cDNA deposited under ATCC No. 40394 or an immunologically reactive fragment thereof of at least 8 contiguous amino acid residues;
  - (b) incubating said antigen with a biological sample under conditions that allow for formation of an antibody-antigen complex; and
  - (c) detecting any antibody-antigen complexes comprised of said antigen.
2. The immunoassay of claim 1 wherein the antigen has been produced through recombinant DNA expression or chemical synthesis.
3. The immunoassay of claims 1 or 2 wherein the biological sample is selected from blood, plasma, and serum.
4. The immunoassay of claim 3 wherein the antigen is attached to a solid support.
5. The immunoassay of claim 4 wherein the solid support is a microtiter plate.
6. The immunoassay of claim 4 wherein the antigen-antibody complexes are detected by incubating the complexes with a labeled anti-immunoglobulin antibody.
7. The immunoassay of claim 6 wherein the anti-immunoglobulin antibody is radiolabeled.
8. The immunoassay of claim 6 wherein the anti-immunoglobulin antibody is enzyme labeled.
9. An immunoassay for detecting antibodies that bind to an HCV polypeptide comprising:
  - (a) providing an antigen comprising a polypeptide selected from the group consisting of (i) a polypeptide consisting of a sequence of amino acid residues 1 to 84, amino acid residues 9 to 177, or amino acid residues 1 to 120 of FIG. 90 and (ii) immunologically reactive fragments of polypeptide (i) of at least 8 contiguous amino acid residues;
  - (b) incubating said antigen with a biological sample under conditions that allow for

formation of an antibody-antigen complex; and

(c) detecting any antibody-antigen complex comprised of said antigen.

10. The immunoassay of claim 9 wherein the antigen comprises a polypeptide having the sequence of amino acid residues 1 to 84 of FIG. 90.
11. The immunoassay of claim 9 wherein the antigen comprises a polypeptide having the sequence of amino acid residues 9 to 177 of FIG. 90.
12. The immunoassay of claim 9, wherein the antigen comprises a polypeptide having the sequence of amino acid residues 1 to 120 of FIG. 90.
13. The immunoassay of claim 9 wherein the antigen comprises an immunologically reactive fragment of at least 8 contiguous amino acid residues from a sequence selected from the group of amino acid residues 1 to 84 or amino acid residues 9 to 177 of FIG. 90.
14. The immunoassay of claim 13 wherein the contiguous amino acid residues comprise a sequence of amino acid residues 35 to 45 of FIG. 90.
15. The immunoassay of claim 13 wherein the contiguous amino acid residues comprise a sequence of amino acid residues 50 to 100 of FIG. 90.
16. The immunoassay of claim 13 wherein the contiguous amino acid residues comprise a sequence of amino acid residues 40 to 90 of FIG. 90.
17. The immunoassay of claim 13 wherein the contiguous amino acid residues comprise a sequence of amino acid residues 65 to 75 of FIG. 90.
18. The immunoassay of claim 13 wherein the contiguous amino acid residues comprise a sequence of amino acid residues 80 to 90 of FIG. 90.
19. The immunoassay of claim 13 wherein the contiguous amino acid residues comprise a sequence of amino acid residues 99 to 120 of FIG. 90.
20. The immunoassay of claim 13 wherein the contiguous amino acid residues comprise a sequence of amino acid residues 95 to 110 of FIG. 90.
21. The immunoassay of claim 13 wherein the contiguous amino acid residues comprise a sequence of amino acid residues 100 to 150 of FIG. 90.
22. The immunoassay of any one of claims 9, 13, 14, 17 or 18 wherein the immunologically active fragment of polypeptide (i) is at least 15 contiguous amino acid residues.
23. The immunoassay of any one of claims 9 to 21 wherein the antigen is attached to a solid support.
24. The immunoassay of claim 22 wherein the antigen is attached to a solid support.
25. The immunoassay of any one of claims 9 to 21 wherein the antigen has been produced through recombinant DNA expression or chemical synthesis.
26. The immunoassay of claim 22 wherein the antigen has been produced through recombinant DNA expression or chemical synthesis.
27. The immunoassay of claim 23 wherein the antigen has been produced through recombinant DNA expression or chemical synthesis.
28. The immunoassay of claim 24 wherein the antigen has been produced through recombinant DNA expression or chemical synthesis.
29. The immunoassay of any one of claims 9 to 21 wherein the biological sample is selected from the group consisting of blood, plasma and serum.
30. The immunoassay of claim 22 wherein the biological sample is selected from the

group consisting of blood, plasma and serum.

31. The immunoassay of claim 24 wherein the biological sample is selected from the group consisting of blood, plasma and serum.
32. The immunoassay of claim 29 wherein the antigen-antibody complexes are detected by incubating the complexes with a labeled anti-immunoglobulin antibody.
33. The immunoassay of claim 30 wherein the antigen-antibody complexes are detected by incubating the complexes with a labeled anti-immunoglobulin antibody.
34. The immunoassay of claim 31 wherein the antigen-antibody complexes are detected by incubating the complexes with a labeled anti-immunoglobulin antibody.
35. The immunoassay of claim 34 wherein the anti-immunoglobulin antibody is radiolabeled.
36. The immunoassay of claim 34 wherein the anti-immunoglobulin is enzyme-labeled.
37. A kit for an immunoassay for detecting antibodies that bind to a hepatitis C virus (HCV) polypeptide comprising an antigen in a suitable container, wherein the antigen is comprised of the C domain polypeptide encoded by HCV cDNA deposited under ATCC No. 40394 or an immunologically reactive fragment thereof of at least 8 contiguous amino acid residues and wherein the antigen is attached to a solid support.
38. A kit for an immunoassay for detecting antibodies that bind to a hepatitis C virus (HCV) polypeptide comprising an antigen in a suitable container, wherein the antigen is comprised of a polypeptide selected from the group consisting of (i) a polypeptide consisting of a sequence of amino acid residues 1 to 84 and amino acid residues 9 to 177 of FIG. 90 and (ii) an immunologically reactive fragment of polypeptide (i) of at least 8 contiguous amino acid residues and wherein the antigen is attached to a solid support.
39. A kit according to claim 38 wherein the antigen is comprised of the sequence of amino acid residues 35 to 45 of FIG. 90.
40. A kit according to any one of claims 37 to 39 wherein the contiguous sequence is at least 15 amino acids residues.
41. A kit according to claim 40 wherein the solid support is a microtiter plate.

US-PAT-NO: 5863719

DOCUMENT-IDENTIFIER: US 5863719 A

TITLE: Methods for detecting hepatitis C virus using polynucleotides specific for same

DATE-ISSUED: January 26, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
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Choo; Qui-Lim	El Cerrito	CA	N/A	N/A
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Kuo; George	San Francisco	CA	N/A	N/A
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US-CL-CURRENT: 435/5,435/6 ,435/91.1 ,435/91.2 ,536/23.72 ,536/24.3

CLAIMS:

We claim:

1. A method for detecting an HCV sequence in a test sample suspected of containing an HCV polynucleotide, wherein the HCV polynucleotide comprises a selected target region, said method comprising:
  - (a) providing an oligonucleotide capable of selectively and detectably hybridizing to the genome of a hepatitis C virus (HCV) or its complement, wherein the oligonucleotide comprises a contiguous sequence of at least 10 nucleotides complementary to the genome of an HCV or its complement;
  - (b) incubating the test sample with the oligonucleotide of step (a) under conditions which allow hybrid duplexes to form between the oligonucleotide and the target region specifically relative to other viral agents; and
  - (c) detecting any hybrids formed between the target region and the oligonucleotide, wherein the presence of said hybrid duplex is indicative of HCV being present in the test sample.
2. The method of claim 1 wherein the contiguous sequence is at least 12 nucleotides.
3. The method of claim 1 wherein the contiguous sequence is at least 15 nucleotides.
4. The method of claim 1 wherein the contiguous sequence is at least 20 nucleotides.
5. The method of claim 1 wherein the contiguous sequence is present in the region beginning at nucleotide -319 and ending at nucleotide 8866 in one of the strands of FIG. 1.
6. The method of claim 1 wherein the contiguous sequence is present in the region beginning at nucleotide 3795 and ending at nucleotide 6373 in one of the strands of FIG. 1.

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DOCUMENT-IDENTIFIER: US 5698390 A

TITLE: Hepatitis C immunoassays

DATE-ISSUED: December 16, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
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US-CL-CURRENT: 435/5,436/518,436/820

CLAIMS:

We claim:

1. An immunoassay for detecting an antibody that binds to a hepatitis C virus (HCV) polypeptide, comprising:
  - (a) providing a polypeptide comprising an amino acid sequence of at least 8 contiguous amino acids encoded by the HCV genome and bindable by said antibody;
  - (b) incubating a biological sample with said polypeptide under conditions that allow for the formation of antibody-antigen complex; and
  - (c) determining whether an antibody-antigen complex comprising said HCV polypeptide is formed.
2. An immunoassay according to claim 1, wherein said biological sample is selected from human blood, serum or plasma.
3. An immunoassay according to claim 1, wherein said polypeptide is prepared by chemical synthesis.
4. An immunoassay according to claim 1, wherein said polypeptide is prepared by recombinant DNA expression.
5. An immunoassay according to claim 1, wherein said polypeptide is attached to a solid support.
6. An immunoassay according to claim 1, wherein said antibody-antigen complexes are detected by incubating the complexes with a labeled anti-human immunoglobulin antibody.
7. An immunoassay of claim 6, wherein said anti-human immunoglobulin is enzyme labeled.
8. An immunoassay according to claim 1, wherein said contiguous sequence is found in FIG. 90.
9. An immunoassay according to claim 1, wherein said contiguous sequence is found in FIG. 47.
10. An immunoassay according to claim 1, wherein said contiguous sequence is found in FIG. 14.
11. An immunoassay according to claim 1, wherein said contiguous sequence is found in FIG. 66.

12. An immunoassay according to claim 1, wherein said contiguous sequence is encoded within the lambda-gt11 CDNA library deposited with the American Type Culture Collection (ATCC) under accession no. 40394.
13. An immunoassay according to any one of claims 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12, wherein said contiguous sequence is at least 10 amino acids.
14. An immunoassay according to any one of claims 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12, wherein said contiguous sequence is at least 15 amino acids.
15. An immunoassay according to claim 1, claim 8, claim 9, claim 10, claim 11, or claim 12, wherein said contiguous sequence is from a nonstructural viral protein.
16. An immunoassay according to claim 1, claim 8, claim 11, or claim 12 wherein said contiguous sequence is from a structural viral protein.
17. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 437 to 582 of the HCV polyprotein.
18. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 511 to 690 of the HCV polyprotein.
19. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 1192 to 1457 of the HCV polyprotein.
20. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 1266 to 1428 of the HCV polyprotein.
21. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 1694 to 1735 of the HCV polyprotein.
22. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 1689 to 1805 of the HCV polyprotein.
23. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 1916 to 2021 of the HCV polyprotein.
24. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 1949 to 2124 of the HCV polyprotein.
25. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 2054 to 2223 of the HCV polyprotein.
26. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 2200 to 2325 of the HCV polyprotein.
27. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 2287 to 2385 of the HCV polyprotein.
28. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 2348 to 2464 of the HCV polyprotein.
29. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 2371 to 2502 of the HCV polyprotein.
30. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 2796 to 2886 of the HCV polyprotein.
31. An immunoassay according to claim 1, or claim 11, wherein said contiguous sequence is found in amino acids 1569 to 1931 of the HCV polyprotein.
32. An immunoassay according to claim 1 or claim 8 wherein said contiguous sequence is found in amino acid 2945 to the carboxy terminus of the HCV polyprotein.
33. An immunoassay according to claim 1, claim 8, or claim 11, wherein said contiguous sequence is selected from the following group:

AA150-AA200; AA200-AA250; AA220-AA240; AA245-AA265; AA250-AA300;  
AA290-AA330;  
AA290-AA305; AA300-AA-350; AA310-AA330; AA350-AA400; AA405-AA495;  
AA400-AA450;  
AA437-AA582; AA450-AA500; AA475-AA495; AA500-AA550; AA511-AA690;  
AA515-AA550;  
AA550-AA600; AA550-AA625; AA575-AA605; AA600-AA650; AA600-AA625;  
AA635-AA665;  
AA650-AA700; AA645-AA680; AA700-AA750; AA700-AA725; AA725-AA775;  
AA770-AA790;  
AA750-AA800; AA800-AA815; AA850-AA875; AA800-AA850; AA920-AA990;  
AA850-AA900;  
AA920-AA945; AA940-AA965; AA950-AA1000; AA1000-AA1060; AA1000-AA1050;  
AA1025-AA1040; AA1075-AA1175-AA1000; AA1000-AA1060; AA1000-AA1050;  
AA1025-AA1040; AA1075-AA1175; AA1050-AA1200; AA1070-AA1100;  
AA1100-AA1140;  
AA1192-AA1457; AA1195-AA1250; AA1200-AA1225; AA1225-AA1250;  
AA1250-AA1300;  
AA1260-AA1310; AA1260-AA1280; AA1266-AA1428; AA1300-AA1350;  
AA1310-AA1340;  
AA1345-AA1405; AA1350-AA1400; AA1365-AA1380; AA1380-AA1405;  
AA1400-AA1450;  
AA1450-AA1500; AA1475-AA1515; AA1475-AA1500; AA1500-AA1550;  
AA1515-AA1550;  
AA1550-AA1600; AA1569-AA1931; AA1570-AA1590; AA1595-AA1610;  
AA1590-AA1650;  
AA1610-AA1645; AA1650-AA1690; AA1685-AA1770; AA1689-AA1805;  
AA1690-AA1720;  
AA1694-AA1735; AA1720-AA1745; AA1745-AA1770; AA1750-AA1800;  
AA1775-AA1810;  
AA1795-AA1850; AA1850-AA1900; AA1900-AA1950; AA1900-AA1920;  
AA1916-AA2021;  
AA1920-AA1940; AA1949-AA2124; AA1950-AA2000; AA1950-AA1985;  
AA2000-AA2050;  
AA2020-AA2045; AA2045-AA2100; AA2045-AA2070; AA2054-AA2223;  
AA2070-AA2100;  
AA2100-AA2150; AA2150-AA2220; AA2200-AA2345; AA2250-AA2330;  
AA2265-AA2280;  
AA2280-AA2290; AA2287-AA2385; AA2300-AA2350; AA2350-AA2400;  
AA2345-AA2415;  
AA2345-AA2375; AA2348-AA2464; AA2370-AA2410; AA2400-AA2450;  
AA2400-AA2425;  
AA2415-AA2450; AA2445-AA2500; AA2371-AA2502; AA2500-AA2550;  
AA2505-AA2540;  
AA2550-AA2600; AA2560-AA2580; AA2600-AA2650; AA2620-AA2650;

AA2650-AA2700;

AA2655-AA2670; AA2670-AA2700; AA2700-AA2750; AA2750-AA2800;

AA2755-AA2780;

AA2780-AA2830; AA2785-AA2810; AA2796-AA2886; AA2810-AA2825;

AA2800-AA2850;

AA2850-AA2900; AA2900-AA2950; AA2910-AA2930; and AA2925-AA2950;

wherein the contiguous amino acid sequence is depicted according to the formula

AA.<sub>sub.x</sub>-AA.<sub>sub.y</sub>, x and y denoting amino acid numbers in the HCV polyprotein.

34. An immunoassay according to claim 33 wherein the contiguous amino acid sequence is found in AA310-AA330.

35. An immunoassay according to claim 33 wherein the contiguous amino acid sequence is found in AA1195-AA1250.

36. An immunoassay according to claim 33 wherein the contiguous amino acid sequence is found in AA1900-AA1950.

37. An immunoassay according to claim 33, wherein the contiguous amino acid sequence is found in AA1900-AA1920.

38. An immunoassay according to claim 33, wherein the contiguous amino acid sequence is found in AA1920-AA1940.

39. An immunoassay according to claim 33, wherein the contiguous amino acid sequence is found in AA2200-AA2345.

40. An immunoassay according to claim 33, wherein the contiguous amino acid sequence is found in AA2280-AA2290.

41. An in vitro diagnostic method for the detection of the presence or absence of human antibodies which bind to an antigen of a hepatitis C virus (HCV), wherein said antigen comprises an HCV polypeptide or an immunologically reactive fragment thereof, and wherein said method comprises:

contacting said HCV polypeptide or immunologically reactive fragment thereof with a biological fluid for a time and under conditions sufficient for the antigen and antibodies in the biological fluid to form antigen-antibody complexes; and detecting the formation of the antigen-antibody complexes containing said HCV polypeptide or immunologically reactive fragment thereof.

42. A method according to claim 41, wherein the biological fluid is blood, serum or plasma.

43. The method of claim 41, wherein the antigen is prepared by chemical synthesis.

44. The method of claim 41, wherein the antigen is prepared by recombinant DNA expression.

45. The method of claim 41, wherein the antigen is fixed to a support.

46. The method of claim 41, wherein the antibody-antigen complexes are detected by incubating the complexes with a labeled anti-human immunoglobulin antibody.

47. The method of claim 46, wherein the anti-human immunoglobulin is enzyme labeled.

48. A method according to claim 41, wherein said immunologically reactive fragment is selected from the following group:

AA150-AA200; AA200-AA250; AA220-AA240; AA245-AA265; AA250-AA300; AA290-AA330;

AA290-AA305; AA300-AA-350; AA310-AA330; AA350-AA400; AA405-AA495;  
AA400-AA450;  
AA437-AA582; AA450-AA500; AA475-AA495; AA500-AA550; AA511-AA690;  
AA515-AA550;  
AA550-AA600; AA550-AA625; AA575-AA605; AA600-AA650; AA600-AA625;  
AA635-AA665;  
AA650-AA700; AA645-AA680; AA700-AA750; AA700-AA725; AA725-AA775;  
AA770-AA790;  
AA750-AA800; AA800-AA815; AA850-AA875; AA800-AA850; AA920-AA990;  
AA850-AA900;  
AA920-AA945; AA940-AA965; AA950-AA1000; AA1000-AA1060; AA1000-AA1050;  
AA1025-AA1040; AA1075-AA1175-AA1000; AA1000-AA1060; AA1000-AA1050;  
AA1025-AA1040; AA1075-AA1175; AA1050-AA1200; AA1070-AA1100;  
AA1100-AA1140;  
AA1192-AA1457; AA1195-AA1250; AA1200-AA1225; AA1225-AA1250;  
AA1250-AA1300;  
AA1260-AA1310; AA1260-AA1280; AA1266-AA1428; AA1300-AA1350;  
AA1310-AA1340;  
AA1345-AA1405; AA1350-AA1400; AA1365-AA1380; AA1380-AA1405;  
AA1400-AA1450;  
AA1450-AA1500; AA1475-AA1515; AA1475-AA1500; AA1500-AA1550;  
AA1515-AA1550;  
AA1550-AA1600; AA1569-AA1931; AA1570-AA1590; AA1595-AA1610;  
AA1590-AA1650;  
AA1610-AA1645; AA1650-AA1690; AA1685-AA1770; AA1689-AA1805;  
AA1690-AA1720;  
AA1694-AA1735; AA1720-AA1745; AA1745-AA1770; AA1750-AA1800;  
AA1775-AA1810;  
AA1795-AA1850; AA1850-AA1900; AA1900-AA1950; AA1900-AA1920;  
AA1916-AA2021;  
AA1920-AA1940; AA1949-AA2124; AA1950-AA2000; AA1950-AA1985;  
AA2000-AA2050;  
AA2020-AA2045; AA2045-AA2100; AA2045-AA2070; AA2054-AA2223;  
AA2070-AA2100;  
AA2100-AA2150; AA2150-AA2220; AA2200-AA2345; AA2250-AA2330;  
AA2265-AA2280;  
AA2280-AA2290; AA2287-AA2385; AA2300-AA2350; AA2350-AA2400;  
AA2345-AA2415;  
AA2345-AA2375; AA2348-AA2464; AA2370-AA2410; AA2400-AA2450;  
AA2400-AA2425;  
AA2415-AA2450; AA2445-AA2500; AA2371-AA2502; AA2500-AA2550;  
AA2505-AA2540;  
AA2550-AA2600; AA2560-AA2580; AA2600-AA2650; AA2620-AA2650;  
AA2650-AA2700;  
AA2655-AA2670; AA2670-AA2700; AA2700-AA2750; AA2750-AA2800;

AA2755-AA2780;

AA2780-AA2830; AA2785-AA2810; AA2796-AA2886; AA2810-AA2825;

AA2800-AA2850;

AA2850-AA2900; AA2900-AA2950; AA2910-AA2930; and AA2925-AA2950;

wherein said immunologically reactive fragment is depicted according to the formula

AA.sub.x -AA.sub.y, x and y denoting amino acid numbers in the HCV polyprotein.

49. A method according to claim 41, wherein said immunologically reactive fragment is from amino acid 2945 to the carboxy terminus of the HCV polyprotein.

50. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 437 to 582 of the HCV polyprotein.

51. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 511 to 690 of the HCV polyprotein.

52. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 1192 to 1457 of the HCV polyprotein.

53. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 1266 to 1428 of the HCV polyprotein.

54. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 1694 to 1735 of the HCV polyprotein.

55. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 1689 to 1805 of the HCV polyprotein.

56. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 1916 to 2021 of the HCV polyprotein.

57. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 1949 to 2124 of the HCV polyprotein.

58. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 2054 to 2223 of the HCV polyprotein.

59. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 2200 to 3325 of the HCV polyprotein.

60. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 2287 to 2385 of the HCV polyprotein.

61. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 2348 to 2464 of the HCV polyprotein.

62. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 2371 to 2502 of the HCV polyprotein.

63. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 2796 to 2886 of the HCV polyprotein.

64. A method according to claim 41, wherein said immunologically reactive fragment is from amino acids 1569 to 1931 of the HCV polyprotein.

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DOCUMENT-IDENTIFIER: US 5712088 A

TITLE: Methods for detecting Hepatitis C virus using polynucleotides specific for same

DATE-ISSUED: January 27, 1998

INVENTOR-INFORMATION:

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Houghton; Michael	Danville	CA	N/A	N/A
Choo; Qui-Lim	El Cerrito	CA	N/A	N/A
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Weiner; Amy J.	Oakland	CA	N/A	N/A
Han; Jang	Lafayette	CA	N/A	N/A
Urdea; Michael Steven	Alamo	CA	N/A	N/A
Irvine; Bruce Duncan	Concord	CA	N/A	N/A
Kolberg; Janice A.	Richmond	CA	N/A	N/A

US-CL-CURRENT: 435/5,435/6 ,435/91.1 ,435/91.2 ,435/91.32 ,536/23.1 ,536/24.32 ,536/24.33 ,536/25.3

CLAIMS:

We claim:

1. A method for detecting an HCV sequence in a test sample suspected of containing an HCV polynucleotide, wherein the HCV polynucleotide comprises a selected target region, said method comprising:
  - (a) providing an oligonucleotide capable of selectively hybridizing to the genome of a hepatitis C virus (HCV), or its complement, wherein the oligonucleotide comprises a contiguous sequence of at least 8 nucleotides fully complementary to the genome of an HCV or its complement;
  - (b) providing a set of primer oligonucleotides which are printers for the polymerase chain reaction method and which flank the target region;
  - (c) amplifying the target region via a polymerase chain reaction method to obtain an amplified test sample;
  - (d) incubating the amplified test sample with the oligonucleotide of step (a) under conditions which allow hybrid duplexes to form between the oligonucleotide and the target region specifically relative to other viral agents; and
  - (e) detecting any hybrids formed between the target region and the oligonucleotide, wherein the presence of said hybrid duplex is indicative of HCV being present in the test sample.
2. The method of claim 1 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 10 nucleotides fully complementary to the genome of an HCV or its complement.
3. The method of claim 1 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 12 nucleotides fully complementary to the genome of

an HCV or its complement.

4. The method of claim 1 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 15 nucleotides fully complementary to the genome of an HCV or its complement.

5. The method of claim 1 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 20 nucleotides fully complementary to the genome of an HCV or its complement.

6. The method of claim 1 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 10 nucleotides fully complementary to a nucleotide residue sequence present in one of the strands of FIG. 1.

7. The method of claim 1 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 10 nucleotides fully complementary to a unique nucleotide residue sequence of the genome of an HCV or its compliment.

8. The method of claim 1 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 12 nucleotides fully complementary to a unique nucleotide residue sequence of the genome of an HCV or its complement.

9. The method of claim 1 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 15 nucleotides fully complementary to a unique nucleotide residue sequence of the genome of an HCV or its complement.

10. The method of claim 1 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 20 nucleotides fully complementary to a unique nucleotide residue sequence of the genome of an HCV or its complement.

11. The method of claim 1 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 10 nucleotides fully complementary to a unique nucleotide residue sequence present in one of the strands of FIG. 1.

12. The method of claim 1 wherein the contiguous sequence is a conserved HCV nucleotide sequence.

13. The method of claim 1 wherein the oligonucleotide provided in step (a) comprises a sequence selected from the group consisting of:

5'-TCC CTT GCT CGA TGT ACG GTA AGT GCT GAG AGC ACT CTT CCA TCT CAT CGA ACT CTC GGT

AGA GGA CTT CCC TGT CAG GT-3',

5'-CTG TCA GGT ATG ATT CCC GGC TTC CCG GAC-3',

5'-TTT GGC TAG TGG TTA GTG GGC TGG TGA CAG-3',

5'-AAG CCA CCG TGT GCG CTA GGG CTC AAG CCC-3',

5'-CAG GAT GCT GTC TCC CGC ACT CAA CGT-3',

5'-AGT GCA GTG GAT GAA CCG GCT GAT AGC CTT-3',

5'-TCC TGA GGC GAC TGC ACC AGT GGA TAA GCT-3',

5'-CAG GAT GCT GTC TCC CGC ACT CAA CGT C-3',

5'-ATC AGG ACC GGG GTG AGA ACA ATT ACC ACT-3',

5'-AGA GAC AAC CAT GAG GTC CCC GGT GTT C-3',

5'-TCG GAC CTT TAC CTG GTC ACG AGG CAC-3',

5'-ACC TTC CCC ATT AAT GCC TAC ACC ACG GGC-3',

5'-TCC ATC TCT CAA GGC AAC TTG CAC CGC TAA-3',

5'-TCC ATG GCT GTC CGC TTC CAC CTC CAA AGT-3',

5'-GCG ACA ATA CGA CAA CAT CCT CTG AGC CCG-3',  
5'-AGC AGA CAA GGG GCC TCC TAG GGT GCA TAA T-3',  
5'-CAC CTA TGT TTA TAA CCA TCT CAC TCC TCT-3',  
5'-CTC TGT CAC CAT ATT ACA AGC GCT ATA TCA-3',  
5'-CTC GTT GCT ACG TCA CCA CAA TTT GGT GTA-3',  
5'-TGC TTG TGG ATG ATG CTA CTC ATA TCC CAA-3',  
'-AGC AGC GGC GTC AAA AGT GAA GGC TAA CTT-3',  
5'-TTC TCG TAT GAT ACC CGC TGC TTT GAC TCC-3',  
5'-TGT GTG GCG ACG ACT TAG TCG TTA TCT GTG-3',  
5'-CAC ACT CCA GTC AAT TCC TGG CTA GGC AAC-3',  
5'-CTG GCT TGA AGA ATC-3',  
5'-AGT TAG GCT GGT GAT TAT GC-3',  
5'-GAA CGT TGC GAT CTG GAA GAC AGG GAC AGG-3',  
5'-TAT CAG TTA TGC CAA CGG AAG CGG CCC CGA-3',  
5'-CTG GTT AGC AGO GCT TTT CTA TCA CCA CAA-3',  
5'-AAG GTC CTG GTA GTG CTG CTG CTA TTT GCC-3',  
5'-ACT GGA CGA CGC AAG GTT GCA ATT GCT CTA-3',  
5'-TTC GAC GTC ACA TCG ATC TGC TTG TCG GGA-3',  
5'-GGT GAC GTG GGT TTC-3',  
5'-GGC TTT ACC ACG TCA CCA ATG ATT GCC CTA-3',  
5'-TTT GGG TAA GGT CAT CGA TAC CCT TAC GTG-3',  
5'-GAA GCC GCA CGT AAG-3',  
5'-CCG GCG TAG GTC GCG CAA TTT GGG TAA-3',  
5'-TCA GAT CGT TGG TGG AGT TTA CTT GTT GCC-3',  
5'-CCA TAG TGG TCT GCG GAA CCG GTG AGT ACA-3',  
5'-ATT GCG AGA TCT ACG GGG CCT GCT ACT CCA-3',  
5'-ATA GCG GCC CTC GAT TGC GAG AGC TAC-3',  
5'-AAT TCG GGC GGC CGC CAT ACG A-3',  
5'-CTT GAT CTA CCT CCA ATC ATT CAA AGA CTC-3',  
5'-TCT TCA ACT GGG CAG TAA GAA CAA AGC TCA-3',  
5'-AAT TCG CGG CCG CCA TAC GAT TTA GGT GAC ACT ATA GAA T15-3',  
5'-TTC GCG GCC GCT ACA GCG GGG GAG ACA T-3',  
'-AAT TCG CGG CCG CCA TAC GA-3',  
5'-CGA TGA AGG TTG GGG TAA ACA CTC CGG CCT-3',  
5'-GAT CCT GGA ATT CTG ATA AGA CCT TAA GAC TAT TTT AA-3',  
5'-AAT TTG GGA ATT CCA TAA TGA GAC CCT TAA GGT ATT ACT CAG CT-3',  
5'-GAG TGC TCA AGC TTC AAA ACA AAA TGG CTC ACT TTC TAT CCC AGA CAA  
AGC AGA GT-3',  
5'-GAG TGC TCG ACT CAT TAG GGG GAA ACA TGG TTC CCC CGG GAG GCG AA-3',  
5'-GAG TGC TCA AGC TTC AAA ACA AAA TGG GGC TCT ACC ACG TCA CCA ATG  
ATT GCC CTA  
AC-3',  
5'-GAG TGC TCG TCG ACT CAT TAA GGG GAC CAG TTC ATC ATC ATA TCC CAT  
GCC AT-3',  
5'-GAG TGC AGC TTC AAA ACA AAA TGA GCA CGA ATC CTA AAC CTC AAA AAA

AAA AC-3',  
5'-GAG TGC TCG TCG ACT CAT TAA CCC AAA TTG CGC GAG CTA CGC CGG GGG  
TCT GT-3',  
5'-GAG TGC TCA AGC TTA CAA AAC AAA ATG GCA CCA GGC GCC AAG CAG AAC  
GTC CAG CTG  
ATC-3',  
5'-GAG TGC TCC TCG AGG TCG ACT CAT TAC TCG GAC CTG TCC CTA TCT TCC  
AGA TCG CAA  
CG-3',  
5'-GGA TCC GCT AGC GGC GCC AAG CAG AAC GTC CAG CTG ATC AAC ACC-3',  
5'-GGA TCC AAG CTT TTA CTC GGA CCT GTC CCT ATC TTC CAG ATC GCA ACG-3',  
5'-CAA TCA TAC CTG ACA G-3',  
'-GAT AAC CTC TGC CTG A-3',  
5'-GCA TGT CAT GAT GTA T-3',  
5'-ACA ATA CTG GTG TCA C-3',  
5'-CCA GCG GTG GCC TGG TAT TG-3',  
5'-TTT GGG TAA GGT CAT CGA TAC CCT TAC GTG-3',  
5'-ATA TGC GGC CGC CTT CCG TTG GAC TAA-3',  
5'-AAT TCG CGG CCG CCA TAC GAT TTA GGT GAC ACT ATA GAA CCC CCC CCC  
CCC CCC-3',  
5'-CGA CAA GAA AGA CAG A-3',  
5'-CGT TGG CAT AAC TGA T-3',  
5'-CTC TAT GGC AAT GAG G-3',  
5'-AGC TTC GAC GTC ACA T-3',  
5'-CTT GAA TTC GCA ATT TGG GTA AGG TCA TCG ATA CCC TTA CG-3',  
5'-CTT GAA TTC GAT AGA GCA ATT GCA ACC TTG CGT CGT CC-3',  
5'-CTT GAA TTC GGA CGA CGC AAG GTT GCA ATT GCT CTA TC-3',  
5'-CTT GAA TTC CAG CCG GTG TTG AGG CTA TCA TTG CAG TTC-3',  
5'-TGA ACT ATG CAA CAG G-3',  
5'-GGA GTG TGC AGG ATG G-3',  
5'-AAG GTT GCA ATT GCT C-3',  
5'-ACT AAC AGG ACC TTC G-3',  
5'-TAA CGG GTC ACC GCA T-3',  
5'-GTA ATA TGG TGA CAG AGT CA-3',  
5'-GAT CTC TAG AGA AAT CAA TAT GGT GAC AGA GTC A-3', and  
5'-CCC AGC GGC GTA CGC GCT GGA CAC GGA GGT GGC CGC GTC GTG TGG CGG  
TGT TGT TCT CGT  
CGG GTT GAT GGC GC-3'.

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DOCUMENT-IDENTIFIER: US 5766845 A

TITLE: Immunoreactive polypeptide compositions

DATE-ISSUED: June 16, 1998

INVENTOR-INFORMATION:

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Houghton; Michael	Danville	CA	N/A	N/A

US-CL-CURRENT: 435/5,424/184.1 ,424/185.1 ,424/189.1 ,424/204.1 ,424/228.1 ,530/300  
,530/324

CLAIMS:

What is claimed is:

1. An in vitro diagnostic method for detecting the presence of or absence of human antibodies to a hepatitis C virus (HCV) comprising the steps of: contacting a biological sample suspected of containing antibodies to HCV with an immunoreactive polypeptide composition, wherein said immunoreactive polypeptide composition comprises at least two HCV amino acid sequences, each HCV sequence comprising at least one epitope within a variable domain of an HCV envelope protein, wherein the variable domain regions of the amino acid sequences are heterogeneous with each other, are derived from distinct HCV isolates, and are encoded from about amino acid 384 to about amino acid 414 of the HCV polyprotein or encoded from about amino acid 215 to about acid 255 of the HCV polyprotein, for a time and under conditions sufficient for the polypeptide composition and antibodies in the biological sample to form antigen-antibody complexes; and detecting the formation of the antigen-antibody complexes containing said immunogenic polypeptides.
2. The method of claim 1, wherein the immunoreactive polypeptide composition comprises a plurality of antigen sets, wherein (a) each antigen set consists of a plurality of substantially identical sequences comprising at least one epitope within a variable domain of an HCV polypeptide and (b) the amino acid sequence of the epitope of one set is heterogeneous with respect to the amino acid sequence of the analogous sequence of at least one other set.
3. A method according to either of claims 1 or 2, wherein the distinct HCV isolates include an HCV group I isolate and an HCV group II isolate.
4. A method according to either of claims 1 or 2, wherein the variable domain is selected from the group consisting of the E1 or E2/NS1 domain of the HCV genome.
5. The method of claim 4, wherein the variable domain is from the E1 domain of the HCV genome.
6. The method of claim 4, wherein the variable domain is from the E2/NS1 domain of the HCV genome.
7. A kit for detecting antibodies to a hepatitis C virus (HCV) within a biological

sample comprising an immunoreactive polypeptide composition comprising at least two HCV amino acid sequences, each HCV sequence comprising at least one epitope within a variable domain of an HCV envelope protein, wherein the variable domain regions of the amino acid sequences are heterogeneous with each other are derived from distinct HCV isolates, and are encoded from about amino acid 384 to about amino acid 414 of the HCV polyprotein or encoded from about amino acid 215 to about acid 255 of the HCV polyprotein, wherein said composition is packaged in a suitable container.

8. A method according to claim 1 wherein the variable domain is encoded from about amino acid 396 to about amino acid 407 of the HCV polyprotein.

9. A method according to claim 1 wherein the variable domain is encoded from about amino acid 396 to about amino acid 408 of the HCV polyprotein.

10. A method according to claim 1 wherein the variable domain is encoded from amino acid 399 to amino acid 406 of the HCV polyprotein.

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DOCUMENT-IDENTIFIER: US 5714596 A

TITLE: NANBV diagnostics: polynucleotides useful for screening for hepatitis C virus

DATE-ISSUED: February 3, 1998

INVENTOR-INFORMATION:

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Kuo; George	San Francisco	CA	N/A	N/A
Weiner; Amy J.	Oakland	CA	N/A	N/A
Han; Jang	Lafayette	CA	N/A	N/A
Urdea; Michael Steven	Alamo	CA	N/A	N/A
Irvine; Bruce Duncan	Concord	CA	N/A	N/A
Kolberg; Janice A.	Richmond	CA	N/A	N/A

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CLAIMS:

What is claimed is:

1. A purified preparation of an oligonucleotide, wherein the oligonucleotide is capable of selectively hybridizing to the genome of a hepatitis C virus (HCV), or its complement, relative to other viral agents, and further wherein the oligonucleotide comprises a contiguous sequence of at least 10 nucleotides fully complementary to either strand of the nucleotide residue sequence depicted in FIG. 1.
2. The purified preparation of claim 1 wherein the oligonucleotide comprises a contiguous sequence of at least 12 nucleotides fully complementary to either strand of the nucleotide residue sequence depicted in FIG. 1.
3. The purified preparation of claim 2 wherein the oligonucleotide is a primer for a DNA polymerase or a reverse transcriptase.
4. The purified preparation of claim 1 wherein the oligonucleotide comprises a contiguous sequence of at least 15 nucleotides fully complementary to either strand of the nucleotide residue sequence depicted in FIG. 1.
5. The purified preparation of claim 1 wherein the oligonucleotide comprises a contiguous sequence of at least 20 nucleotides fully complementary to either strand of the nucleotide residue sequence depicted in FIG. 1.
6. The purified preparation of claim 1 wherein the oligonucleotide is a primer for DNA polymerase or a reverse transcriptase.
7. The purified preparation of claim 1 wherein the contiguous sequence is a conserved HCV nucleotide sequence.
8. The purified preparation of claim 7 wherein the conserved sequence is located in

the sequence of nucleotide numbers from the 5' terminus to 200 in FIG. 1.

9. The purified preparation of claim 7 wherein the conserved sequence is located in the sequence of nucleotide numbers from 4000 to 5000 in FIG. 1.

10. The purified preparation of claim 7 wherein the conserved sequence is located in the sequence of nucleotide numbers from 8000 to 9040 in FIG. 1.

11. The purified preparation of claim 7 wherein the conserved sequence is located in the sequence of nucleotide numbers from -318 to 174 in FIG. 1.

12. The purified preparation of claim 7 wherein the conserved sequence is located in the sequence of nucleotide numbers from 4056 to 4448 in FIG. 1.

13. The purified preparation of claim 7 wherein the conserved sequence is located in the sequence of nucleotide numbers from 4378 to 4902 in FIG. 1.

14. The purified preparation of claim 7 wherein the conserved sequence is located in the sequence of nucleotide numbers from 4042 to 4059 in FIG. 1.

15. The purified preparation of claim 7 wherein the conserved sequence is located in the sequence of nucleotide numbers from 4456 to 4470 in FIG. 1.

16. The purified preparation of claim 7 wherein the conserved sequence is located in the sequence of nucleotide numbers from 8209 to 8217 in FIG. 1.

17. The purified preparation of claim 1, wherein the oligonucleotide hybridizes to the sequence of nucleotide numbers from -313 to -282 in FIG. 1.

18. The purified preparation of claim 1 wherein the oligonucleotide hybridizes to the sequence of nucleotide numbers from -203 to -173 in FIG. 1.

19. The purified preparation of claim 1, wherein the oligonucleotide hybridizes to the sequence of nucleotide numbers from -252 to -221 in FIG. 1.

20. The purified preparation of claim 1, wherein the oligonucleotide hybridizes to a sequence located between nucleotide 16 and nucleotide 486 in FIG. 1.

21. The purified preparation of claim 1 wherein the oligonucleotide comprises a sequence selected from the group consisting of:

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TCC CTT  
GCT CGA TGT ACG GTA AGT GCT GAG AGC ACT CTT CCA TCT CAT CGA ACT CTC  
GGT AGA GGA CTT  
CCC TGT CAG GT - 3', CTG TCA GGT ATG ATT GCC GGC TTC CCG GAC - 3', TTT  
GGC TAG TGG  
TTA GTG GGC TGG TGA CAG - 3', AAG CCA CCG TGT GCG CTA GGG CTC AAG CCC-  
3', CAG GAT  
GCT GTC TCC CGC ACT CAA CGT - 3', AGT GCA GTG GAT GAA CCG GCT GAT AGC  
CTT - 3',  
TCC TGA GGC GAC TGC ACC AGT GGA TAA GCT - 3', CAG GAT GCT GTC TCC CGC  
ACT CAA CGT C  
- 3', ATC AGG ACC GGG GTG AGA ACA ATT ACC ACT - 3', AGA GAC AAC CAT GAG  
GTC CCC  
GGT GTT C - 3', TCG GAC CTT TAC CTG GTC ACG AGG CAC - 3', ACC TTC CCC ATT  
AAT GCC  
TAC ACC ACG GGC - 3', TCC ATC TCT CAA GGC AAC TTG CAC CGC TAA - 3', TCC  
ATG GCT

GTC CGC TTC CAC CTC CAA AGT - 3', GCG ACA ATA CGA CAA CAT CCT CTG AGC CCG - 3',  
AGC AGA CAA GGG GCC TCC TAG GGT GCA TAA T - 3', CAC CTA TGT TTA TAA CCA TCT CAC TCC  
TCT - 3', CTC TGT CAC CAT ATT ACA AGC GCT ATA TCA - 3', CTC GTT GCT ACG TCA CCA  
CAA TTT GGT GTA - 3', TGC TTG TGG ATG ATG CTA CTC ATA TCC CAA - 3', AGC AGC GGC  
GTC AAA AGT GAA GGC TAA CTT - 3', TTC TCG TAT GAT ACC CGC TGC TTT GAC TCC - 3',  
TGT GTG GCG ACG ACT TAG TCG TTA TCT GTG - 3', CAC ACT CCA GTC AAT TCC TGG CTA GGC  
AAC - 3', CTG GCT TGA AGA ATC - 3', AGT TAG GCT GGT GAT TAT GC - 3', GAA CGT TGC  
GAT CTG GAA GAC AGG GAC AGG - 3', TAT CAG TTA TGC CAA CGG AAG CGG CCC CGA - 3',  
CTG GTT AGC AGG GCT TTT CTA TCA CCA CAA - 3', AAG GTC CTG GTA GTG CTG CTG CTA TTT  
GCC - 3', ACT GGA CGA CGC AAG GTT GCA ATT GCT CTA - 3', TTC GAC GTC ACA TCG ATC  
TGC TTG TCG GGA - 3', GGT GAC GTG GGT TTC - 3', GGC TTT ACC ACG TCA CCA ATG ATT  
GCC CTA - 3', TTT GGG TAA GGT CAT CGA TAC CCT TAC GTG - 3', GAA GCC GCA CGT AAG -  
3', CCG GCG TAG GTC GCG CAA TTT GGG TAA - 3', TCA GAT CGT TGG TGG AGT TTA CTT GTT  
GCC - 3', CCA TAG TGG TCT GCG GAA CCG GTG AGT ACA - 3', ATT GCG AGA TCT ACG GGG  
CCT GCT ACT CCA - 3', ATA GCG GCC GCC CTC GAT TGC GAG AGC TAC - 3', AAT TCG GGC  
GGC CGC CAT ACG A-3', CTT GAT CTA CCT CCA ATC ATT CAA AGA CTC - 3', TCT TCA ACT  
GGG CAG TAA GAA CAA AGC TCA - 3', AAT TCG CGG CCG CCA TAC GAT TTA GGT GAC ACT ATA  
GAA T.<sub>sub.15</sub> -3', TTC GCG GCC GCT ACA GCG GGG GAG ACA T - 3', AAT TCG CGG CCG CCA  
TAC GA - 3', CGA TGA AGG TTG GGG TAA ACA CTC CGG CCT - 3', GAT CCT GGA ATT CTG ATA  
AGA CCT TAA GAC TAT TTT AA - 3', AAT TTG GGA ATT CCA TAA TGA GAC CCT TAA GGT ATT  
ACT CAG CT - 3', GAG TGC TCA AGC TTC AAA ACA AAA TGG CTC ACT TTC TAT CCC AGA CAA  
AGC AGA GT - 3', GAG TGC TCG ACT CAT TAG GGG GAA ACA TGG TTC CCC CGG GAG GCG  
AA-3', GAG TGC TCA AGC TTC AAA ACA AAA TGG GGC TCT ACC ACG TCA CCA

ATG ATT GCC CTA  
AC - 3', GAG TGC TCG TCG ACT CAT TAA GGG GAC CAG TTC ATC ATC ATA TCC  
CAT GCC AT -  
3', GAG TGC AGC TTC AAA ACA AAA TGA GCA CGA ATC CTA AAC CTC AAA AAA  
AAA AC - 3',  
GAG TGC TCG TCG ACT CAT TAA CCC AAA TTG CGC GAC CTA CGC CGG GGG TCT  
GT - 3' GAG  
TGC TCA AGC TTA CAA AAC AAA ATG GCA CCA GCC GGC AAG CAG AAG GTC  
CAG CTG ATC - 3',  
GAG TGC TCC TCG AGG TCG ACT CAT TAC TCG GAC CTG TCC CTA TCT TCC AGA  
TCG CAA CG -  
3', GGA TCC GCT AGC GGC GCC AAG CAG AAC GTC CAG CTG ATC AAC ACC-3',  
GGA TCC AAG  
CTT TTA CTC GGA CCT GTC CCT ATC TTC CAG ATC GCA ACG - 3', CAA TCA TAC  
CTG ACA G -  
3', GAT AAC CTC TGC CTG A - 3', GCA TGT CAT GAT GTA T - 3', ACA ATA CTG  
GTG TCA C  
- 3', CCA GCG GTG GCC TGG TAT TG - 3', TTT GGG TAA GGT CAT CGA TAC CCT  
TAC GTG -  
3', ATA TGC GGC CGC CTT CCG TTG GAC TAA - 3', AAT TCG CGG CCG CCA TAC  
GAT TTA GGT  
GAC ACT ATA GAA CCC CCC CCC CCC CCC - 3', CGA CAA GAA AGA CAG A - 3',  
CGT TGG CAT  
AAC TGA T - 3', CTC TAT GGC AAT GAG G - 3', AGC TTC GAC GTC ACA T - 3', CTT  
GAA  
TTC GCA ATT TGG GTA AGG TCA TCG ATA CCC TTA CG-3', CTT GAA TTC GAT  
AGA GCA ATT GCA  
ACC TTG CGT CGT CC - 3', CTT GAA TTC GGA CGA CGC AAG GTT GCA ATT GCT  
CTA TC - 3',  
CTT GAA TTC CAG CCG GTG TTG AGG CTA TCA TTG CAG TTC - 3', TGA ACT ATG  
CAA CAG G -  
3', GGA GTG TGC AGG ATG G - 3', AAG GTT GCA ATT GCT C - 3', ACT AAC AGG  
ACC TTC G  
- 3', TAA CGG GTC ACC GCA T - 3', GTA ATA TGG TGA CAG AGT CA - 3', GAT CTC  
TAG  
AGA AAT CAA TAT GGT GAC AGA GTC A - 3', and CCC AGC GGC GTA CGC GCT  
GGA CAC GGA GGT  
GGC CGC GTC GTG TGG CGG TGT TGT TCT CGT CGG GTT GAT GGC GC - 3'.

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22. The purified preparation of claim 1 wherein the oligonucleotide comprises a contiguous sequence of at least 10 nucleotides fully complementary to a unique nucleotide residue sequence in either strand of the nucleotide residue sequence depicted in FIG. 1.

23. The purified preparation of claim 22 wherein the oligonucleotide is a primer for a DNA polymerase or a reverse transcriptase.

24. The purified preparation of claim 1 wherein the oligonucleotide comprises a contiguous sequence of at least 12 nucleotides fully complementary to a unique nucleotide residue sequence in either strand of the nucleotide residue sequence depicted in FIG. 1.
25. The purified preparation of claim 24 wherein the oligonucleotide is a primer for a DNA polymerase or a reverse transcriptase.
26. The purified preparation of claim 1 wherein the oligonucleotide comprises a contiguous sequence of at least 15 nucleotides fully complementary to a unique nucleotide residue sequence in either strand of the nucleotide residue sequence depicted in FIG. 1.
27. The purified preparation of claim 1 wherein the oligonucleotide comprises a contiguous sequence of at least 20 nucleotides fully complementary to a unique nucleotide residue sequence in either strand of the nucleotide residue sequence depicted in FIG. 1.